

SEQUENCE LISTING

<110> Prof. Dr. Axel R. Zander

<120> Use of CD34 or a Polypeptide derived therefrom as
Cell Surface/Gene Transfer Marker

<130> 35-204

<140>

<141>

<160> 10

<170> PatentIn Ver. 2.0

<210> 1

<211> 1122

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1122)

<223> CD34 (complete length)

<400> 1

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1				5					10					15		

ggg	ttc	atg	agt	ctt	gac	aac	aac	ggt	act	gct	acc	cca	gag	tta	cct	96
Gly	Phe	Met	Ser	Leu	Asp	Asn	Asn	Gly	Thr	Ala	Thr	Pro	Glu	Leu	Pro	
			20					25					30			

acc	cag	gga	aca	ttt	tca	aat	gtt	tct	aca	aat	gta	tcc	tac	caa	gaa	144
Thr	Gln	Gly	Thr	Phe	Ser	Asn	Val	Ser	Thr	Asn	Val	Ser	Tyr	Gln	Glu	
		35					40					45				

act	aca	aca	cct	agt	acc	ctt	gga	agt	acc	agc	ctg	cac	cct	gtg	tct	192
Thr	Thr	Thr	Pro	Ser	Thr	Leu	Gly	Ser	Thr	Ser	Leu	His	Pro	Val	Ser	
		50				55					60					

caa	cat	ggc	aat	gag	gcc	aca	aca	aac	atc	aca	gaa	acg	aca	gtc	aaa	240
Gln	His	Gly	Asn	Glu	Ala	Thr	Thr	Asn	Ile	Thr	Glu	Thr	Thr	Val	Lys	
65				70					75						80	

ttc	aca	tct	acc	tct	gtg	ata	acc	tca	gtt	tat	gga	aac	aca	aac	tct	288
Phe	Thr	Ser	Thr	Ser	Val	Ile	Thr	Ser	Val	Tyr	Gly	Asn	Thr	Asn	Ser	
				85					90					95		

tct	gtc	cag	tca	cag	acc	tct	gta	atc	agc	aca	gtg	ttc	acc	acc	cca	336
Ser	Val	Gln	Ser	Gln	Thr	Ser	Val	Ile	Ser	Thr	Val	Phe	Thr	Thr	Pro	

PatentIn Ver. 2.0

gcc aac gtt tca act cca gag aca acc ttg aag cct agc ctg tca cct	384
Ala Asn Val Ser Thr Pro Glu Thr Thr Leu Lys Pro Ser Leu Ser Pro	
115 120 125	
gga aat gtt tca gac ctt tca acc act agc act agc ctt gca aca tct	432
Gly Asn Val Ser Asp Leu Ser Thr Thr Ser Thr Ser Leu Ala Thr Ser	
130 135 140	
ccc act aaa ccc tat aca tca tct tct cct atc cta agt gac atc aag	480
Pro Thr Lys Pro Tyr Thr Ser Ser Ser Pro Ile Leu Ser Asp Ile Lys	
145 150 155 160	
gca gaa atc aaa tgt tca ggc atc aga gaa gtg aaa ttg act cag ggc	528
Ala Glu Ile Lys Cys Ser Gly Ile Arg Glu Val Lys Leu Thr Gln Gly	
165 170 175	
atc tgc ctg gag caa aat aag acc tcc agc tgt gcg gag ttt aag aag	576
Ile Cys Leu Glu Gln Asn Lys Thr Ser Ser Cys Ala Glu Phe Lys Lys	
180 185 190	
gac agg gga gag ggc ctg gcc cga gtg ctg tgt ggg gag gag cag gct	624
Asp Arg Gly Glu Gly Leu Ala Arg Val Leu Cys Gly Glu Glu Gln Ala	
195 200 205	
gat gct gat gct ggg gcc cag gta tgc tcc ctg ctc ctt gcc cag tct	672
Asp Ala Asp Ala Gly Ala Gln Val Cys Ser Leu Leu Leu Ala Gln Ser	
210 215 220	
gag gtg agg cct cag tgt cta ctg ctg gtc ttg gcc aac aga aca gaa	720
Glu Val Arg Pro Gln Cys Leu Leu Leu Val Leu Ala Asn Arg Thr Glu	
225 230 235 240	
att tcc agc aaa ctc caa ctt atg aaa aag cac caa tct gac ctg aaa	768
Ile Ser Ser Lys Leu Gln Leu Met Lys Lys His Gln Ser Asp Leu Lys	
245 250 255	
aag ctg ggg atc cta gat ttc act gag caa gat gtt gca agc cac cag	816
Lys Leu Gly Ile Leu Asp Phe Thr Glu Gln Asp Val Ala Ser His Gln	
260 265 270	
agc tat tcc caa aag acc ctg att gca ctg gtc acc tcg gga gcc ctg	864
Ser Tyr Ser Gln Lys Thr Leu Ile Ala Leu Val Thr Ser Gly Ala Leu	
275 280 285	
ctg gct gtc ttg ggc atc act ggc tat ttc ctg atg aat cgc cgc agc	912
Leu Ala Val Leu Gly Ile Thr Gly Tyr Phe Leu Met Asn Arg Arg Ser	
290 295 300	
tgg agc ccc aca gga gaa agg ctg ggc gaa gac cct tat tac acg gaa	960
Trp Ser Pro Thr Gly Glu Arg Leu Gly Glu Asp Pro Tyr Tyr Thr Glu	
305 310 315 320	
aac ggt gga ggc cag ggc tat agc tca gga cct ggg acc tcc cct gag	1008
Asn Gly Gly Gly Gln Gly Tyr Ser Ser Gly Pro Gly Thr Ser Pro Glu	
325 330 335	

Leu	Ala	Val	Leu	Gly	Ile	Thr	Gly	Tyr	Phe	Leu	Met	Asn	Arg	Arg	Ser
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Trp	Ser	Pro	Thr	Gly	Glu	Arg	Leu	Gly	Glu	Asp	Pro	Tyr	Tyr	Thr	Glu
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Asn	Gly	Gly	Gly	Gln	Gly	Tyr	Ser	Ser	Gly	Pro	Gly	Thr	Ser	Pro	Glu
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Ala	Gln	Gly	Lys	Ala	Ser	Val	Asn	Arg	Gly	Ala	Gln	Glu	Asn	Gly	Thr
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Gly	Gln	Ala	Thr	Ser	Arg	Asn	Gly	His	Ser	Ala	Arg	Gln	His	Val	Val
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 <213> Homo sapiens

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 <222> (1)..(951)
 <223> CD34 (truncated variant)

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1				5				10						15		
ggg ttc atg agt ctt gac aac aac ggt act gct acc cca gag tta cct															96	
Gly	Phe	Met	Ser	Leu	Asp	Asn	Asn	Gly	Thr	Ala	Thr	Pro	Glu	Leu	Pro	
			20					25					30			
acc cag gga aca ttt tca aat gtt tct aca aat gta tcc tac caa gaa															144	
Thr	Gln	Gly	Thr	Phe	Ser	Asn	Val	Ser	Thr	Asn	Val	Ser	Tyr	Gln	Glu	
			35				40					45				
act aca aca cct agt acc ctt gga agt acc agc ctg cac cct gtg tct															192	
Thr	Thr	Thr	Pro	Ser	Thr	Leu	Gly	Ser	Thr	Ser	Leu	His	Pro	Val	Ser	
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caa cat ggc aat gag gcc aca aca aac atc aca gaa acg aca gtc aaa															240	
Gln	His	Gly	Asn	Glu	Ala	Thr	Thr	Asn	Ile	Thr	Glu	Thr	Thr	Val	Lys	
					70					75					80	
ttc aca tct acc tct gtg ata acc tca gtt tat gga aac aca aac tct															288	
Phe	Thr	Ser	Thr	Ser	Val	Ile	Thr	Ser	Val	Tyr	Gly	Asn	Thr	Asn	Ser	
				85					90					95		
tct gtc cag tca cag acc tct gta atc agc aca gtg ttc acc acc cca															336	
Ser	Val	Gln	Ser	Gln	Thr	Ser	Val	Ile	Ser	Thr	Val	Phe	Thr	Thr	Pro	
			100					105					110			

gcc aac gtt tca act cca gag aca acc ttg aag cct agc ctg tca cct	384
Ala Asn Val Ser Thr Pro Glu Thr Thr Leu Lys Pro Ser Leu Ser Pro	
115 120 125	
gga aat gtt tca gac ctt tca acc act agc act agc ctt gca aca tct	432
Gly Asn Val Ser Asp Leu Ser Thr Thr Ser Thr Ser Leu Ala Thr Ser	
130 135 140	
ccc act aaa ccc tat aca tca tct tct cct atc cta agt gac atc aag	480
Pro Thr Lys Pro Tyr Thr Ser Ser Ser Pro Ile Leu Ser Asp Ile Lys	
145 150 155 160	
gca gaa atc aaa tgt tca ggc atc aga gaa gtg aaa ttg act cag ggc	528
Ala Glu Ile Lys Cys Ser Gly Ile Arg Glu Val Lys Leu Thr Gln Gly	
165 170 175	
atc tgc ctg gag caa aat aag acc tcc agc tgt gcg gag ttt aag aag	576
Ile Cys Leu Glu Gln Asn Lys Thr Ser Ser Cys Ala Glu Phe Lys Lys	
180 185 190	
gac agg gga gag ggc ctg gcc cga gtg ctg tgt ggg gag gag cag gct	624
Asp Arg Gly Glu Gly Leu Ala Arg Val Leu Cys Gly Glu Glu Gln Ala	
195 200 205	
gat gct gat gct ggg gcc cag gta tgc tcc ctg ctc ctt gcc cag tct	672
Asp Ala Asp Ala Gly Ala Gln Val Cys Ser Leu Leu Leu Ala Gln Ser	
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gag gtg agg cct cag tgt cta ctg ctg gtc ttg gcc aac aga aca gaa	720
Glu Val Arg Pro Gln Cys Leu Leu Leu Val Leu Ala Asn Arg Thr Glu	
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att tcc agc aaa ctc caa ctt atg aaa aag cac caa tct gac ctg aaa	768
Ile Ser Ser Lys Leu Gln Leu Met Lys Lys His Gln Ser Asp Leu Lys	
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Lys Leu Gly Ile Leu Asp Phe Thr Glu Gln Asp Val Ala Ser His Gln	
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agc tat tcc caa aag acc ctg att gca ctg gtc acc tcg gga gcc ctg	864
Ser Tyr Ser Gln Lys Thr Leu Ile Ala Leu Val Thr Ser Gly Ala Leu	
275 280 285	
ctg gct gtc ttg ggc atc act ggc tat ttc ctg atg aat cgc cgc agc	912
Leu Ala Val Leu Gly Ile Thr Gly Tyr Phe Leu Met Asn Arg Arg Ser	
290 295 300	
tgg agc ccc aca gga gaa agg ctg gaa cta gaa cca tga	951
Trp Ser Pro Thr Gly Glu Arg Leu Glu Leu Glu Pro	
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 <213> Homo sapiens

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 35 40 45
 Thr Thr Thr Pro Ser Thr Leu Gly Ser Thr Ser Leu His Pro Val Ser
 50 55 60
 Gln His Gly Asn Glu Ala Thr Thr Asn Ile Thr Glu Thr Thr Val Lys
 65 70 75 80
 Phe Thr Ser Thr Ser Val Ile Thr Ser Val Tyr Gly Asn Thr Asn Ser
 85 90 95
 Ser Val Gln Ser Gln Thr Ser Val Ile Ser Thr Val Phe Thr Thr Pro
 100 105 110
 Ala Asn Val Ser Thr Pro Glu Thr Thr Leu Lys Pro Ser Leu Ser Pro
 115 120 125
 Gly Asn Val Ser Asp Leu Ser Thr Thr Ser Thr Ser Leu Ala Thr Ser
 130 135 140
 Pro Thr Lys Pro Tyr Thr Ser Ser Ser Pro Ile Leu Ser Asp Ile Lys
 145 150 155 160
 Ala Glu Ile Lys Cys Ser Gly Ile Arg Glu Val Lys Leu Thr Gln Gly
 165 170 175
 Ile Cys Leu Glu Gln Asn Lys Thr Ser Ser Cys Ala Glu Phe Lys Lys
 180 185 190
 Asp Arg Gly Glu Gly Leu Ala Arg Val Leu Cys Gly Glu Glu Gln Ala
 195 200 205
 Asp Ala Asp Ala Gly Ala Gln Val Cys Ser Leu Leu Leu Ala Gln Ser
 210 215 220
 Glu Val Arg Pro Gln Cys Leu Leu Leu Val Leu Ala Asn Arg Thr Glu
 225 230 235 240
 Ile Ser Ser Lys Leu Gln Leu Met Lys Lys His Gln Ser Asp Leu Lys
 245 250 255
 Lys Leu Gly Ile Leu Asp Phe Thr Glu Gln Asp Val Ala Ser His Gln
 260 265 270
 Ser Tyr Ser Gln Lys Thr Leu Ile Ala Leu Val Thr Ser Gly Ala Leu
 275 280 285
 Leu Ala Val Leu Gly Ile Thr Gly Tyr Phe Leu Met Asn Arg Arg Ser
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 Trp Ser Pro Thr Gly Glu Arg Leu Glu Leu Glu Pro
 305 310 315

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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

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210 215 220	
gag gtg agg cct cag tgt cta ctg ctg gtc ttg gcc aac aga aca gaa	720
Glu Val Arg Pro Gln Cys Leu Leu Leu Val Leu Ala Asn Arg Thr Glu	
225 230 235 240	
att tcc agc aaa ctc caa ctt atg aaa aag cac caa tct gac ctg aaa	768
Ile Ser Ser Lys Leu Gln Leu Met Lys Lys His Gln Ser Asp Leu Lys	
245 250 255	
aag ctg ggg atc cta gat ttc act gag caa gat gtt gca agc cac cag	816
Lys Leu Gly Ile Leu Asp Phe Thr Glu Gln Asp Val Ala Ser His Gln	
260 265 270	
agc tat tcc caa aag acc ctg att gca ctg gtc acc tcg gga gcc ctg	864
Ser Tyr Ser Gln Lys Thr Leu Ile Ala Leu Val Thr Ser Gly Ala Leu	
275 280 285	
ctg gct gtc ttg ggc atc act ggc tat ttc ctg atg aat tga	906
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 <213> Homo sapiens

<400> 6

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			20					25					30		
Thr	Gln	Gly	Thr	Phe	Ser	Asn	Val	Ser	Thr	Asn	Val	Ser	Tyr	Gln	Glu
		35					40				45				
Thr	Thr	Thr	Pro	Ser	Thr	Leu	Gly	Ser	Thr	Ser	Leu	His	Pro	Val	Ser
		50				55				60					
Gln	His	Gly	Asn	Glu	Ala	Thr	Thr	Asn	Ile	Thr	Glu	Thr	Thr	Val	Lys
65					70					75					80
Phe	Thr	Ser	Thr	Ser	Val	Ile	Thr	Ser	Val	Tyr	Gly	Asn	Thr	Asn	Ser
				85					90					95	
Ser	Val	Gln	Ser	Gln	Thr	Ser	Val	Ile	Ser	Thr	Val	Phe	Thr	Thr	Pro
			100					105					110		
Ala	Asn	Val	Ser	Thr	Pro	Glu	Thr	Thr	Leu	Lys	Pro	Ser	Leu	Ser	Pro
		115					120					125			
Gly	Asn	Val	Ser	Asp	Leu	Ser	Thr	Thr	Ser	Thr	Ser	Leu	Ala	Thr	Ser
		130				135					140				
Pro	Thr	Lys	Pro	Tyr	Thr	Ser	Ser	Ser	Pro	Ile	Leu	Ser	Asp	Ile	Lys
					150					155					160
Ala	Glu	Ile	Lys	Cys	Ser	Gly	Ile	Arg	Glu	Val	Lys	Leu	Thr	Gln	Gly
				165						170					175

Ile	Cys	Leu	Glu	Gln	Asn	Lys	Thr	Ser	Ser	Cys	Ala	Glu	Phe	Lys	Lys
			180					185					190		
Asp	Arg	Gly	Glu	Gly	Leu	Ala	Arg	Val	Leu	Cys	Gly	Glu	Glu	Gln	Ala
		195					200					205			
Asp	Ala	Asp	Ala	Gly	Ala	Gln	Val	Cys	Ser	Leu	Leu	Leu	Ala	Gln	Ser
	210					215					220				
Glu	Val	Arg	Pro	Gln	Cys	Leu	Leu	Leu	Val	Leu	Ala	Asn	Arg	Thr	Glu
225					230					235					240
Ile	Ser	Ser	Lys	Leu	Gln	Leu	Met	Lys	Lys	His	Gln	Ser	Asp	Leu	Lys
			245						250					255	
Lys	Leu	Gly	Ile	Leu	Asp	Phe	Thr	Glu	Gln	Asp	Val	Ala	Ser	His	Gln
		260						265					270		
Ser	Tyr	Ser	Gln	Lys	Thr	Leu	Ile	Ala	Leu	Val	Thr	Ser	Gly	Ala	Leu
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Leu	Ala	Val	Leu	Gly	Ile	Thr	Gly	Tyr	Phe	Leu	Met	Asn			
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 <212> DNA
 <213> Artificial sequence

<220>
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36

<210> 8
 <211> 31
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: Primer CD34rev

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31

<210> 9
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 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: Primer CD34lrev

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47

$\langle 210 \rangle$ 10

<211> 34

<212> DNA

<213> Artificial sequence

 $\langle 220 \rangle$

<223> Description of the artificial sequence: Primer CD34srev

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34

[illegible]